

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

OCR-754.CIP

Applicants	James M. Anderson and Christina M. Van Itallie
Serial No. - pending	Filing Date: June 25, 2001
Art Unit 1644	Examiner Patrick Nolan
Title of Application	Human Occludin, Its Uses and Enhancement of Drug Absorption Using Occludin Inhibitors

Commissioner of Patents  
and Trademarks  
Washington, DC 20231

**SUBMISSION OF A SEQUENCE STATEMENT UNDER 37 C.F.R. § 1.821(g)**

Dear Sir:

The computer-readable form submitted herewith with an application that is a C.I.P. of U.S. application serial number 09/142,732, filed September 15, 1998, is identical to the Sequence Listing of its parent case and that filed in the international parent case, PCT/US97/05809, filed March 14, 1997, and contains no new matter.

Respectfully submitted,

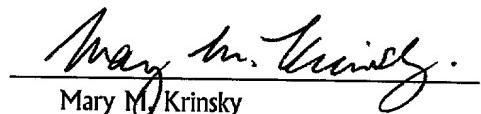
June 25, 2001 by



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I hereby certify that this paper and the application are today being deposited with the United States Postal Service as Express Mail, no. EL572277375US, under 37 C.F.R. § 1.10 in an envelope addressed to the Box New Application, Commissioner of Patents, Washington, D.C. 20231.

June 25, 2001

  
Mary M. Krinsky

1/7  
SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANTS: James M. Anderson  
Christina M. Van Itallie
- (ii) TITLE OF INVENTION: Human Occludin, Its Uses  
and Enhancement of Drug Absorption Using Occludin Inhibitors
- (iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS

- (A) ADDRESSEE: Yale University Medical School  
Section of Pulmonary and Critical Care Medicine  
Department of Internal Medicine
- (B) STREET: 333 Cedar Street, LCI 105
- (C) CITY: New Haven
- (D) STATE: Connecticut
- (E) COUNTRY: United States of America
- (F) ZIP CODE: 065220-8057

(v) COMPUTER READABLE FORM

- (A) MEDIUM TYPE: 3.5" 1.44 Mb diskette
- (B) COMPUTER: IBM PC
- (C) OPERATING SYSTEM: MS DOS
- (D) SOFTWARE: Word Processing

(vi) CURRENT APPLICATION DATA

- (A) APPLICATION NUMBER:
- (B) FILING DATE: June 25, 2001
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA

- (A) APPLICATION NUMBER: U.S. 09/142,732
- (B) FILING DATE: September 15, 1998
- (C) CLASSIFICATION: 530-350.000

(viii) ATTORNEY INFORMATION

- (A) NAME: Mary M. Krinsky
- (B) REGISTRATION NO.: 32423
- (C) REFERENCE/DOCKET NUMBER: OCR-754.CIP

(ix) TELECOMMUNICATION INFORMATION

- (A) TELEPHONE NUMBER: 203-773-9544
- (B) TELEFAX NUMBER: 203-773-1183

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2312
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE:

- (A) DESCRIPTION: cDNA

## (v) FRAGMENT TYPE: complete sequence

## (ix) FEATURE:

- (A) NAME/KEY: human occludin

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GCCTCTCTCC	ATCAGACACC	CCAAGGTTCC	ATCCGAAGCA	GGCGGAGCAC	50
CGAACGCACC	CCGGGGTGGT	CAGGGACCCC	CATCCGTGCT	GCCCCCTAGG	100
AGCCCGCGCC	TCTCCTCTGC	GCCCCGCCTC	TCGGGCCGCA	ACATCGCGCG	150
GTTCCTTAA	CAGCGCGCTG	GCAGGGTGTG	GGAAGCAGGA	CCGCGTCCTC	200
CCGCCCCCTC	CCATCCGAGT	TTCAGGTGAA	TTGGTCACCG	AGGGAGGAGG	250
CCGACACACC	ACACCTACAC	TCCCGCGTCC	ACCTCTCCCT	CCCTGCTTCC	300
TCTTGGCGGA	GGCGGCAGGA	ACCGAGAGCC	AGGTCCAGAG	CGCCGAGGAG	350
CCGGTCTAGG	ACGCAGCAGA	TTGGTTTATC	TTGGAAGCTA	AAGGGCATTG	400
CTCATCCTGA	AGATCAGCTG	ACCATTGACA	ATCAGCCATG	TCATCCAGGC	450
CTCTTGAAAG	TCCACCTCCT	TACAGGCCTG	ATGAATTCAA	ACCGAATCAT	500
TATGCACCAA	GCAATGACAT	ATATGGTGGA	GAGATGCATG	TTCGACCAAT	550
GCTCTCTCAG	CCAGCCTACT	CTTTTACCC	AGAAGATGAA	ATTCTTCACT	600
TCTACAAATG	GACCTCTCCT	CCAGGAGTGA	TTCGGATCCT	GTCTATGCTC	650
ATTATTGTGA	TGTGCATTGC	CATCTTGCC	TGTGTGGCCT	CCACGCTTGC	700
CTGGGACAGA	GGCTATGGAA	CTTCCCTTTT	AGGAGGTAGT	GTAGGCTACC	750
CTTATGGAGG	AAGTGGCTTT	GGTAGCTACG	GAAGTGGCTA	TGGCTATGGC	800
TATGGTTATG	GCTATGGCTA	CGGAGGCTAT	ACAGACCCAA	GAGCAGCAAA	850
GGGCTTCATG	TTGGCCATGG	CTGCCTTTG	TTTCATTGCC	GCCTTGTTGA	900
TCTTTGTTAC	CAGTGTATA	AGATCTGAAA	TGTCCAGAAC	AAGAAGATAC	950
TACTTAAGTG	TGATAATAGT	GAGTGCTATC	CTGGGCATCA	TGGTGTATTAT	1000
TGCCACAATT	GTCTATATAA	TGGGAGTGAA	CCCAACTGCT	CAGTCTTCTG	1050
GATCTCTATA	TGGTTCACAA	ATATATGCC	TCTGCAACCA	ATTTTATACA	1100
CCTGCAGCTA	CTGGACTCTA	CGTGGATCAG	TATTTGTATC	ACTACTGTGT	1150
TGTGGATCCC	CAGGAGGCCA	TTGCCATTGT	ACTGGGGTTC	ATGATTATTG	1200

TGGCTTTGC TTTAATAATT TTCTTGCTG TGAAAACTCG AAGAAAGATG 1250  
 GACAGGTATG ACAAGTCCAA TATTTGTGG GACAAGGAAC ACATTTATGA 1300  
 TGAGCAGCCC CCCAATGTCG AGGAGTGGGT TAAAAATGTG TCTGCAGGCA 1350  
 CACAGGACGT GCCTTCACCC CCATCTGACT ATGTGGAAAG AGTTGACAGT 1400  
 CCCATGGCAT ACTCTTCCAA TGGCAAAGTG AATGACAAGC GGTTTTATCC 1450  
 AGAGTCTTCC TATAAATCCA CGCCGGTCC TGAAGTGGTT CAGGAGCTTC 1500  
 CATTAACCTTC GCCTGTGGAT GACTTCAGGC AGCCTCGTTA CAGCAGCGGT 1550  
 GGTAACTTG AGACACCTTC AAAAAGAGCA CCTGCAAAGG GAAGAGCAGG 1600  
 AAGGTCAAAG AGAACAGAGC AAGATCACTA TGAGACAGAC TACACAAC TG 1650  
 GCGGCGAGTC CTGTGATGAG CTGGAGGAGG ACTGGATCAG GGAATATCCA 1700  
 CCTATCACTT CAGATCAACA AAGACAAC TG TACAAGAGGA ATTGACAC 1750  
 TGGCCTACAG GAATACAAGA GCTTACAATC AGAACTTGAT GAGATCAATA 1800  
 AAGAACTCTC CCGTTGGAT AAAGAATTGG ATGACTATAG AGAAGAAAGT 1850  
 GAAGAGTACA TGGCTGCTGC TGATGAATAC AATAGACTGA AGCAAGTGAA 1900  
 GGGATCTGCA GATTACAAAA GTAAGAAGAA TCATTGCAAG CAGTTAAAGA 1950  
 GCAAATTGTC ACACATCAAG AAGATGGTTG GAGACTATGA TAGACAGAAA 2000  
 ACATAGAAGG CTGATGCCAA GTTGTGAG AAATTAAGTA TCTGACATCT 2050  
 CTGCAATCTT CTCAGAAGGC AAATGACTTT GGACCATAAC CCCGGAAGGCC 2100  
 AACACCTCTGT GAGCATCACA AAGTTTGGG TTGCTTTAAC ATCATCAGTA 2150  
 TTGAAGCATT TTATAAATCG CTTTGATAA TCAACTGGGC TGAACAACTC 2200  
 CAATTAAGGA TTTTATGCTT TAAACATTGG TTCTTGTATT AAGAATGAAA 2250  
 TACTGTTGA GGTTTTAACG CCTTAAAGGA AGGTTCTGGT GTGAACAAA 2300  
 CTTTCACACC CC 2312

## (3) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 522
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: polypeptide
- (v) FRAGMENT TYPE: complete sequence
- (ix) FEATURE:
  - (A) NAME/KEY: human occludin

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ser	Ser	Arg	Pro	Leu	Glu	Ser	Pro	Pro	Pro	Tyr	Arg	Pro	Asp
				5				10					15	
Glu	Phe	Lys	Pro	Asn	His	Tyr	Ala	Pro	Ser	Asn	Asp	Ile	Tyr	Gly
				20				25					30	
Gly	Glu	Met	His	Val	Arg	Pro	Met	Leu	Ser	Gln	Pro	Ala	Tyr	Ser
				35				40					45	
Phe	Tyr	Pro	Glu	Asp	Glu	Ile	Leu	His	Phe	Tyr	Lys	Trp	Thr	Ser
				50				55					60	
Pro	Pro	Gly	Val	Ile	Arg	Ile	Leu	Ser	Met	Leu	Ile	Ile	Val	Met
				65				70					75	
Cys	Ile	Ala	Ile	Phe	Ala	Cys	Val	Ala	Ser	Thr	Leu	Ala	Trp	Asp
				80				85					90	
Arg	Gly	Tyr	Gly	Thr	Ser	Leu	Leu	Gly	Gly	Ser	Val	Gly	Tyr	Pro
				95				100					105	
Tyr	Gly	Gly	Ser	Gly	Phe	Gly	Ser	Tyr	Gly	Ser	Gly	Tyr	Gly	Tyr
				110				115					120	
Gly	Tyr	Gly	Tyr	Gly	Tyr	Gly	Tyr	Gly	Gly	Tyr	Thr	Asp	Pro	Arg
				125				130					135	
Ala	Ala	Lys	Gly	Phe	Met	Leu	Ala	Met	Ala	Ala	Phe	Cys	Phe	Ile
				140				145					150	
Ala	Ala	Leu	Val	Ile	Phe	Val	Thr	Ser	Val	Ile	Arg	Ser	Glu	Met
				155				160					165	
Ser	Arg	Thr	Arg	Arg	Tyr	Tyr	Leu	Ser	Val	Ile	Ile	Val	Ser	Ala
				170				175					180	
Ile	Leu	Gly	Ile	Met	Val	Phe	Ile	Ala	Thr	Ile	Val	Tyr	Ile	Met
				185				190					195	
Gly	Val	Asn	Pro	Thr	Ala	Gln	Ser	Ser	Gly	Ser	Leu	Tyr	Gly	Ser
				200				205					210	
Gln	Ile	Tyr	Ala	Leu	Cys	Asn	Gln	Phe	Tyr	Thr	Pro	Ala	Ala	Thr
				215				220					225	
Gly	Leu	Tyr	Val	Asp	Gln	Tyr	Leu	Tyr	His	Tyr	Cys	Val	Val	Asp
				230				235					240	
Pro	Gln	Glu	Ala	Ile	Ala	Ile	Val	Leu	Gly	Phe	Met	Ile	Ile	Val
				245				250					255	

Ala Phe Ala Leu Ile Ile Phe Phe Ala Val Lys Thr Arg Arg Lys  
 260 265 270  
 Met Asp Arg Tyr Asp Lys Ser Asn Ile Leu Trp Asp Lys Glu His  
 275 280 285  
 Ile Tyr Asp Glu Gln Pro Pro Asn Val Glu Glu Trp Val Lys Asn  
 290 295 300  
 Val Ser Ala Gly Thr Gln Asp Val Pro Ser Pro Pro Ser Asp Tyr  
 305 310 315  
 Val Glu Arg Val Asp Ser Pro Met Ala Tyr Ser Ser Asn Gly Lys  
 320 325 330  
 Val Asn Asp Lys Arg Phe Tyr Pro Glu Ser Ser Tyr Lys Ser Thr  
 335 340 345  
 Pro Val Pro Glu Val Val Gln Glu Leu Pro Leu Thr Ser Pro Val  
 350 355 360  
 Asp Asp Phe Arg Gln Pro Arg Tyr Ser Ser Gly Gly Asn Phe Glu  
 365 370 375  
 Thr Pro Ser Lys Arg Ala Pro Ala Lys Gly Arg Ala Gly Arg Ser  
 380 385 390  
 Lys Arg Thr Glu Gln Asp His Tyr Glu Thr Asp Tyr Thr Thr Gly  
 395 400 405  
 Gly Glu Ser Cys Asp Glu Leu Glu Glu Asp Trp Ile Arg Glu Tyr  
 410 415 420  
 Pro Pro Ile Thr Ser Asp Gln Gln Arg Gln Leu Tyr Lys Arg Asn  
 425 430 435  
 Phe Asp Thr Gly Leu Gln Glu Tyr Lys Ser Leu Gln Ser Glu Leu  
 440 445 450  
 Asp Glu Ile Asn Lys Glu Leu Ser Arg Leu Asp Lys Glu Leu Asp  
 455 460 465  
 Asp Tyr Arg Glu Glu Ser Glu Glu Tyr Met Ala Ala Ala Asp Glu  
 470 475 480  
 Tyr Asn Arg Leu Lys Gln Val Lys Gly Ser Ala Asp Tyr Lys Ser  
 485 490 495  
 Lys Lys Asn His Cys Lys Gln Leu Lys Ser Lys Leu Ser His Ile  
 500 505 510  
 Lys Lys Met Val Gly Asp Tyr Asp Arg Gln Lys Thr  
 515 520

## (4) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: peptide
- (v) FRAGMENT TYPE: synthetic peptide
- (ix) FEATURE:
  - (D) OTHER INFORMATION: construct used in experiments
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Cys Asp Arg Gly Tyr Gly Thr Ser Leu Leu Gly Gly Ser Val Gly  
5 10 15

Tyr Pro Tyr Gly Gly Ser Gly Phe Gly  
20

## (5) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: peptide
- (v) FRAGMENT TYPE: synthetic peptide
- (ix) FEATURE:
  - (D) OTHER INFORMATION: construct used in experiments
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Cys Ser Tyr Gly Ser Gly Tyr Gly Tyr Gly Tyr Gly Tyr Gly Tyr  
5 10 15

Gly Tyr Gly Gly Tyr Thr Asp Pro Arg  
20

## (6) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: peptide
- (v) FRAGMENT TYPE: synthetic peptide
- (ix) FEATURE:
  - (D) OTHER INFORMATION: construct used in experiments
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Asn His Tyr Ala Pro Ser Asn Asp Ile Tyr Gly Gly Glu Met Val  
5 10 15

His Arg Pro Met Leu  
20

## (7) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: peptide
- (v) FRAGMENT TYPE: synthetic peptide
- (ix) FEATURE:
  - (D) OTHER INFORMATION: construct used in experiments
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ala Ser Gln Gln Val Tyr Arg Lys Asp Pro Cys  
5 10